

Figure 1

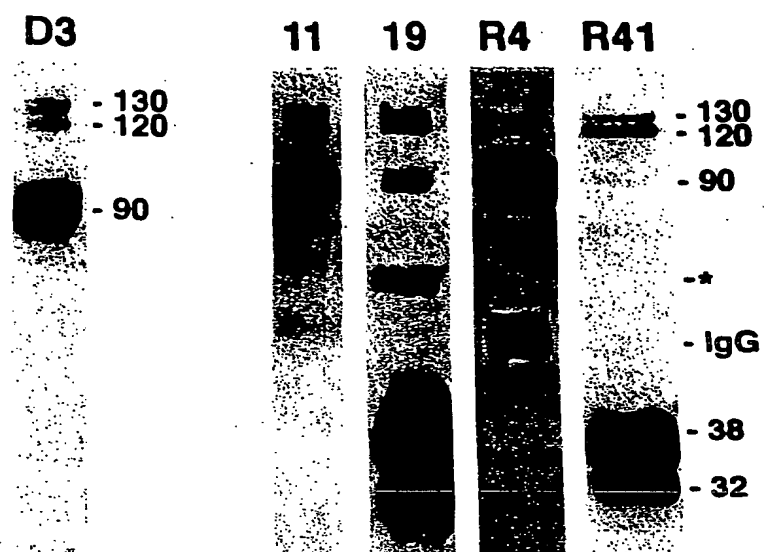


Figure 2A

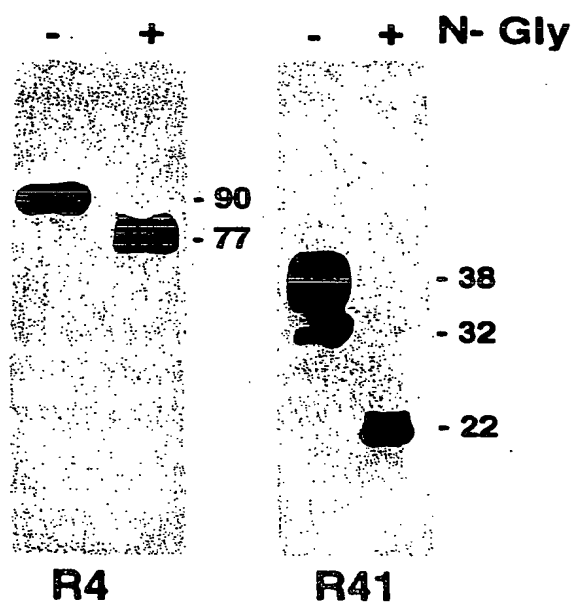


Figure 2B

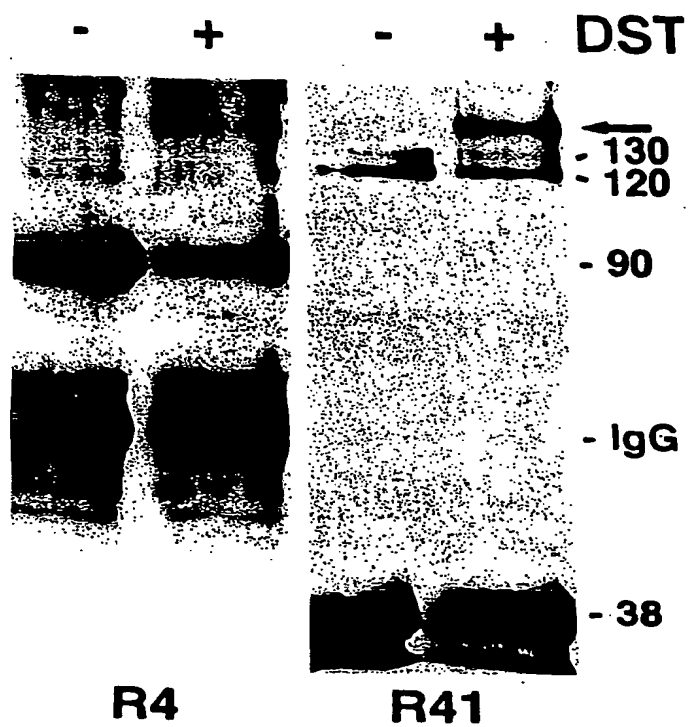


Figure 3A

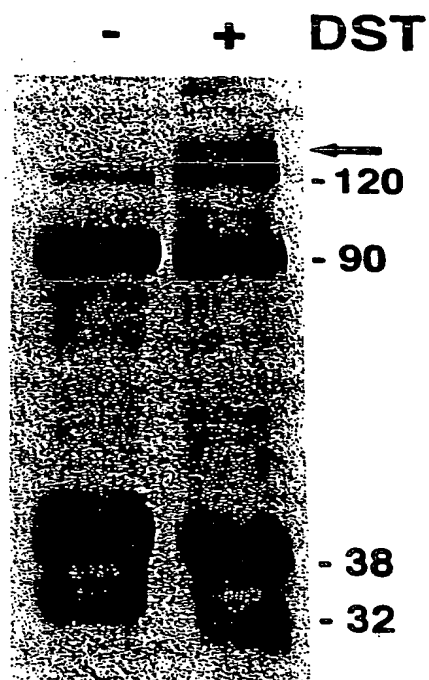
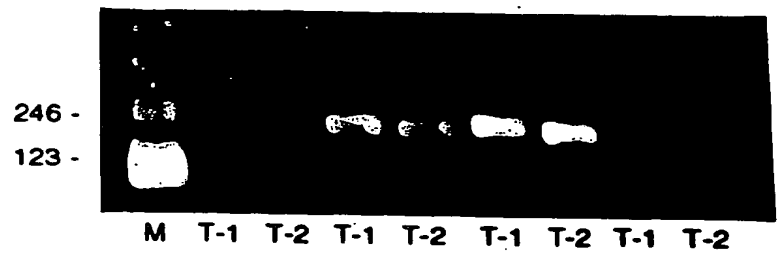


Figure 4A



Figure 4B



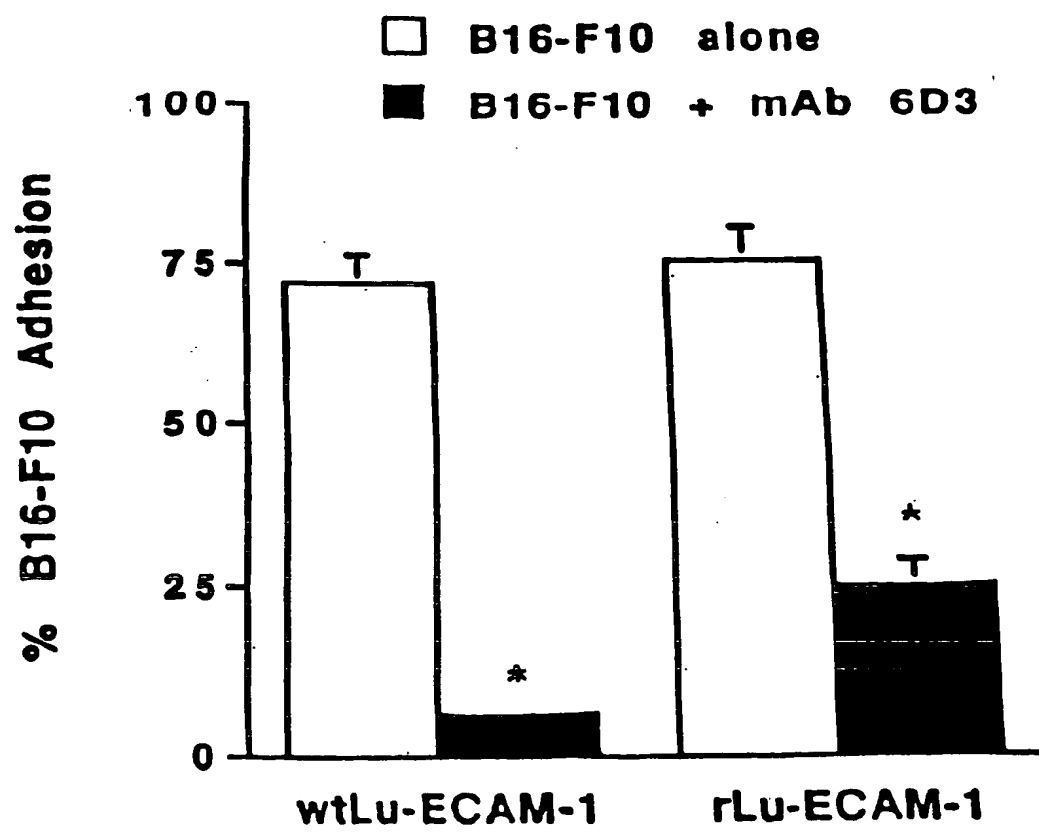


Figure 5

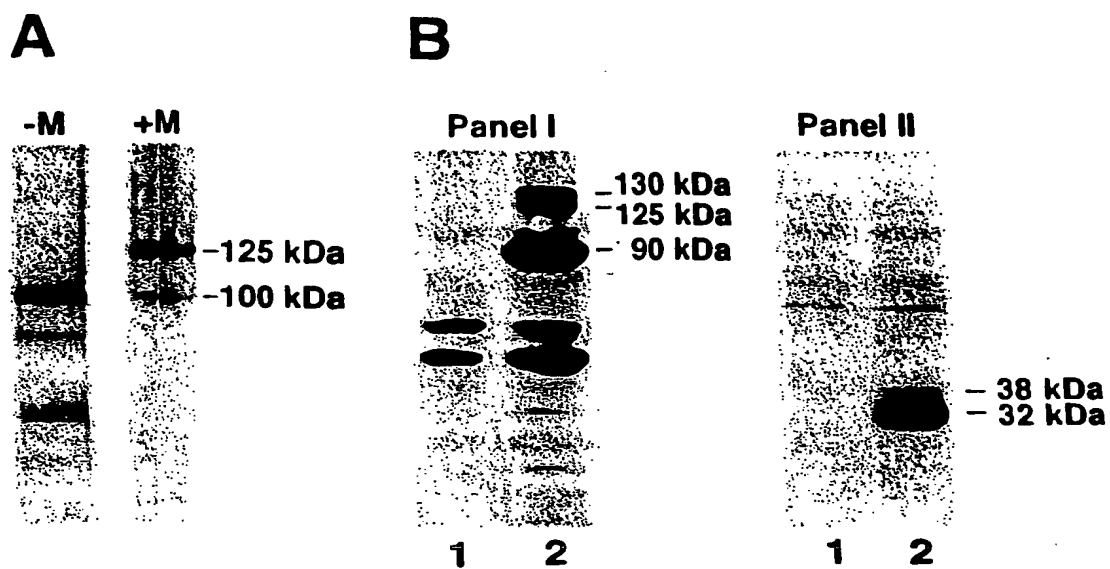


Figure 6

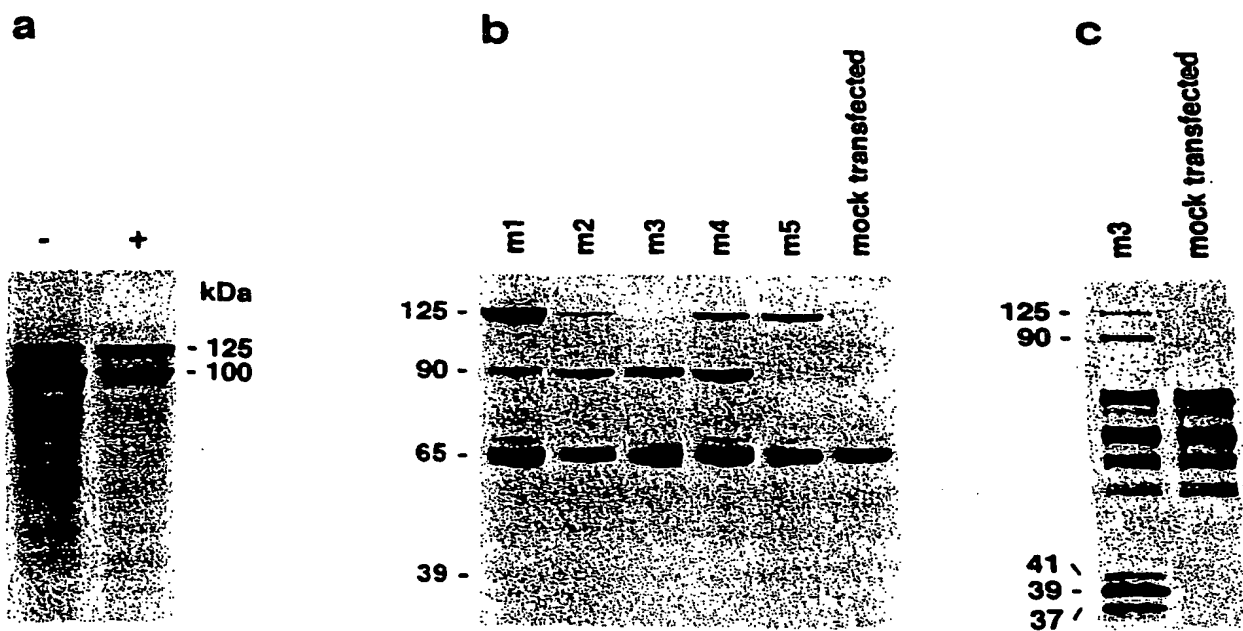


Figure 7

**a**

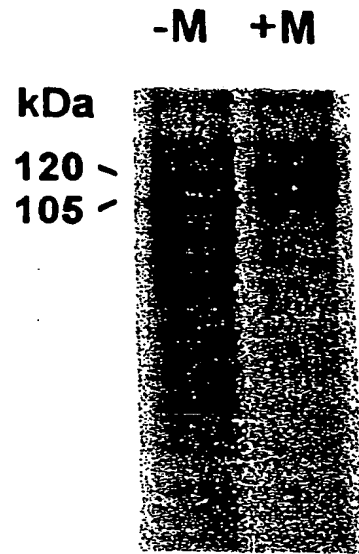
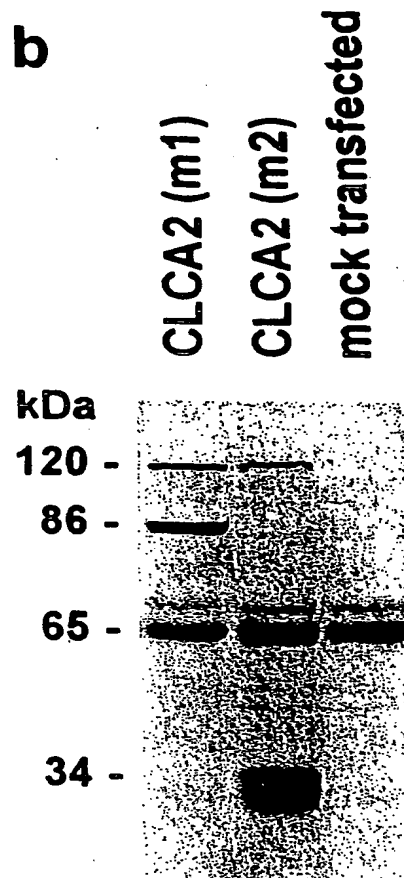


Figure 8

**b**



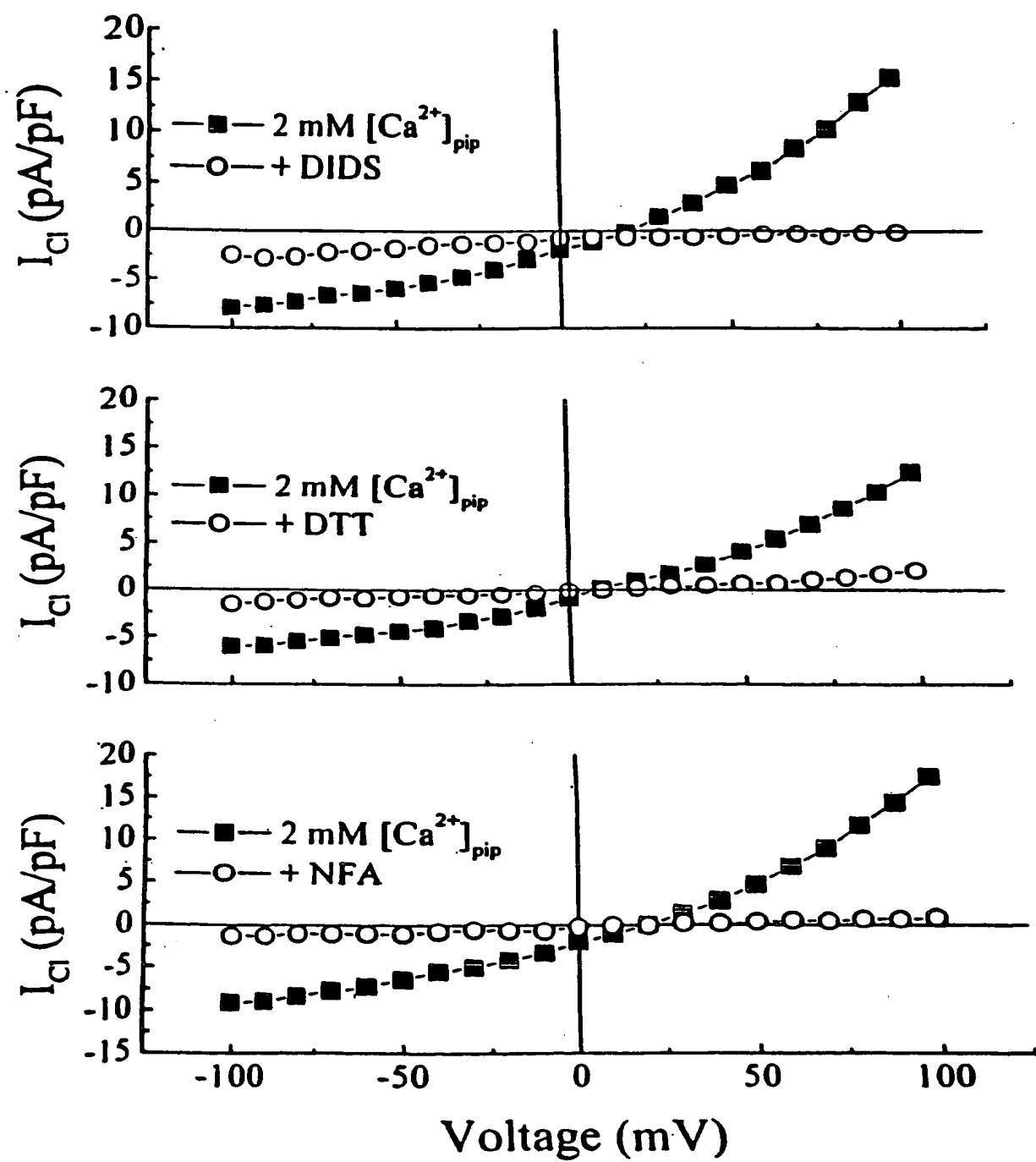


Figure 9



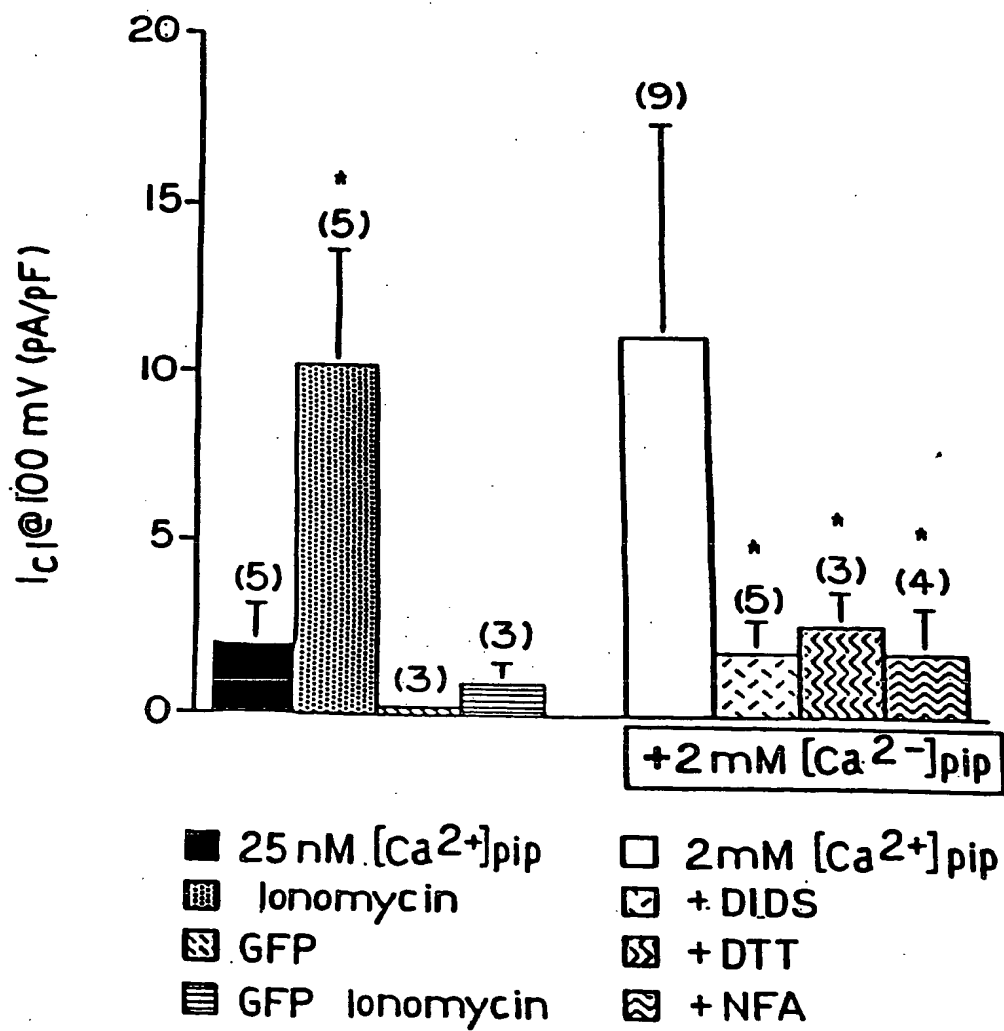
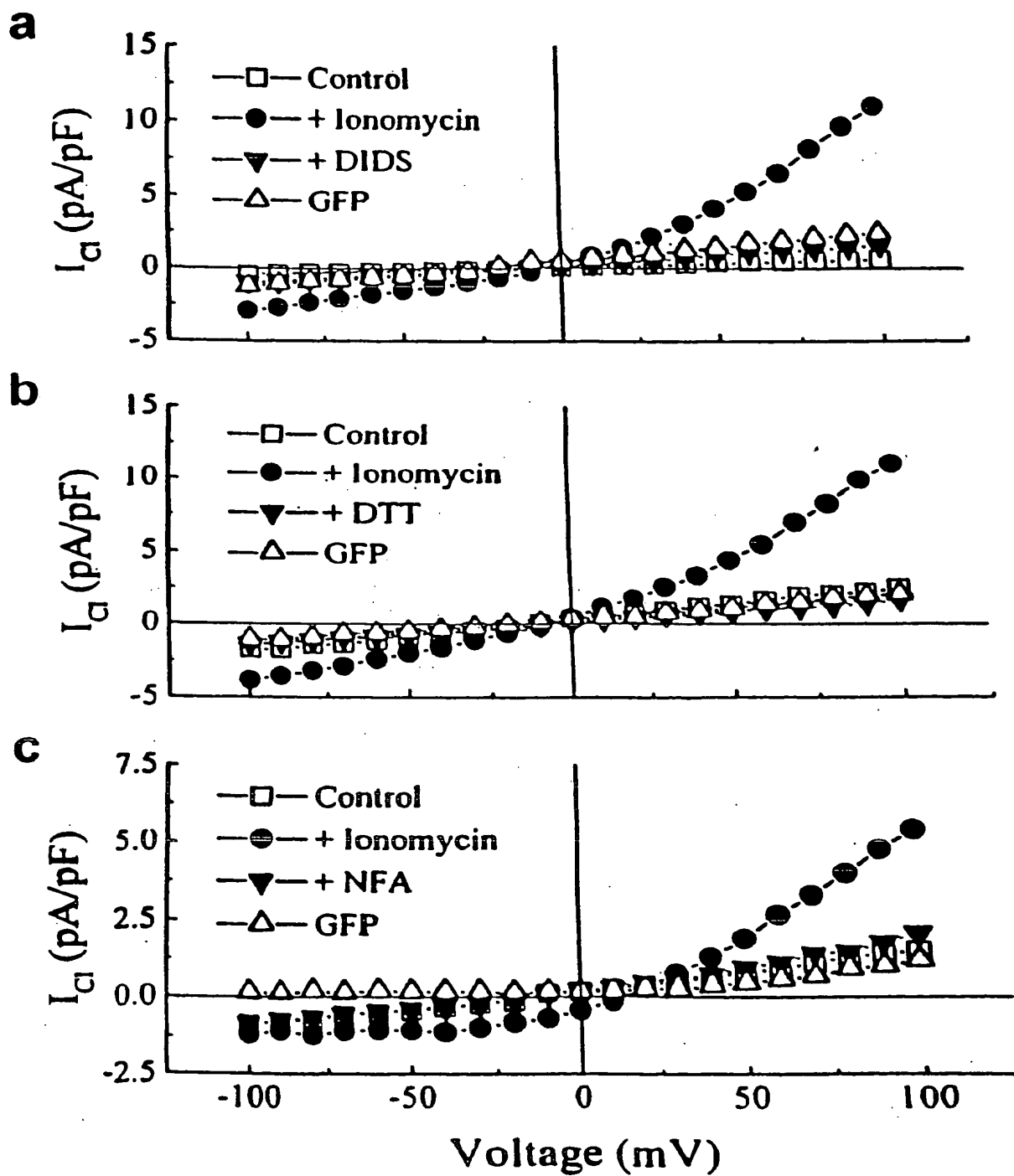


Figure 10

Fig. 11



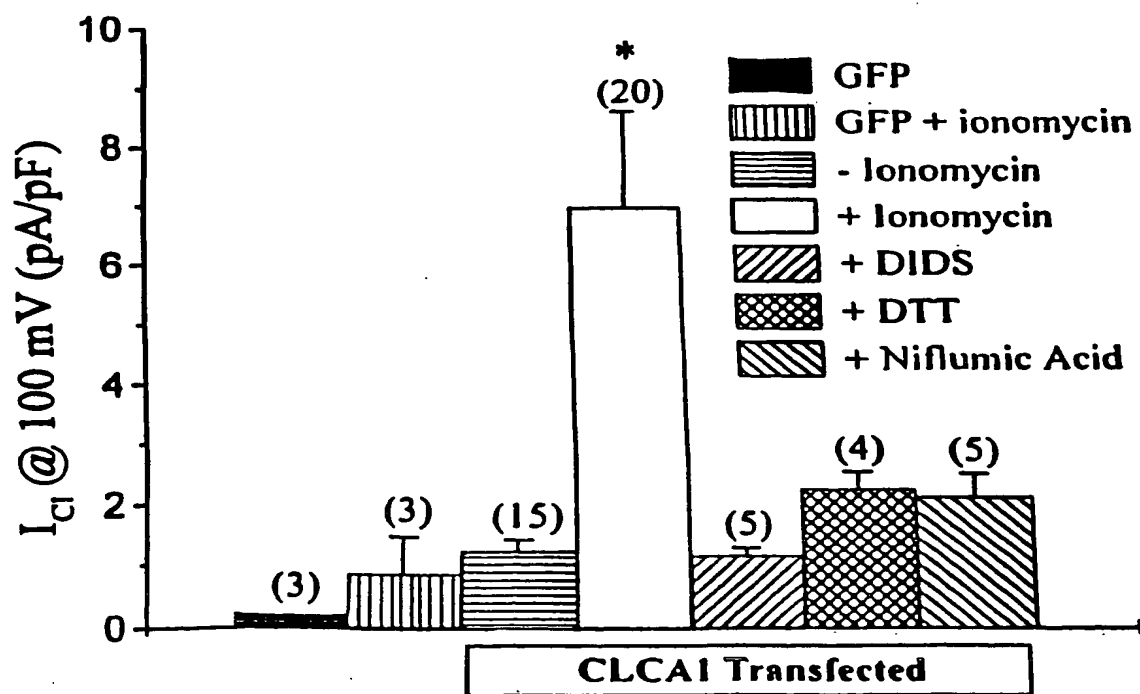
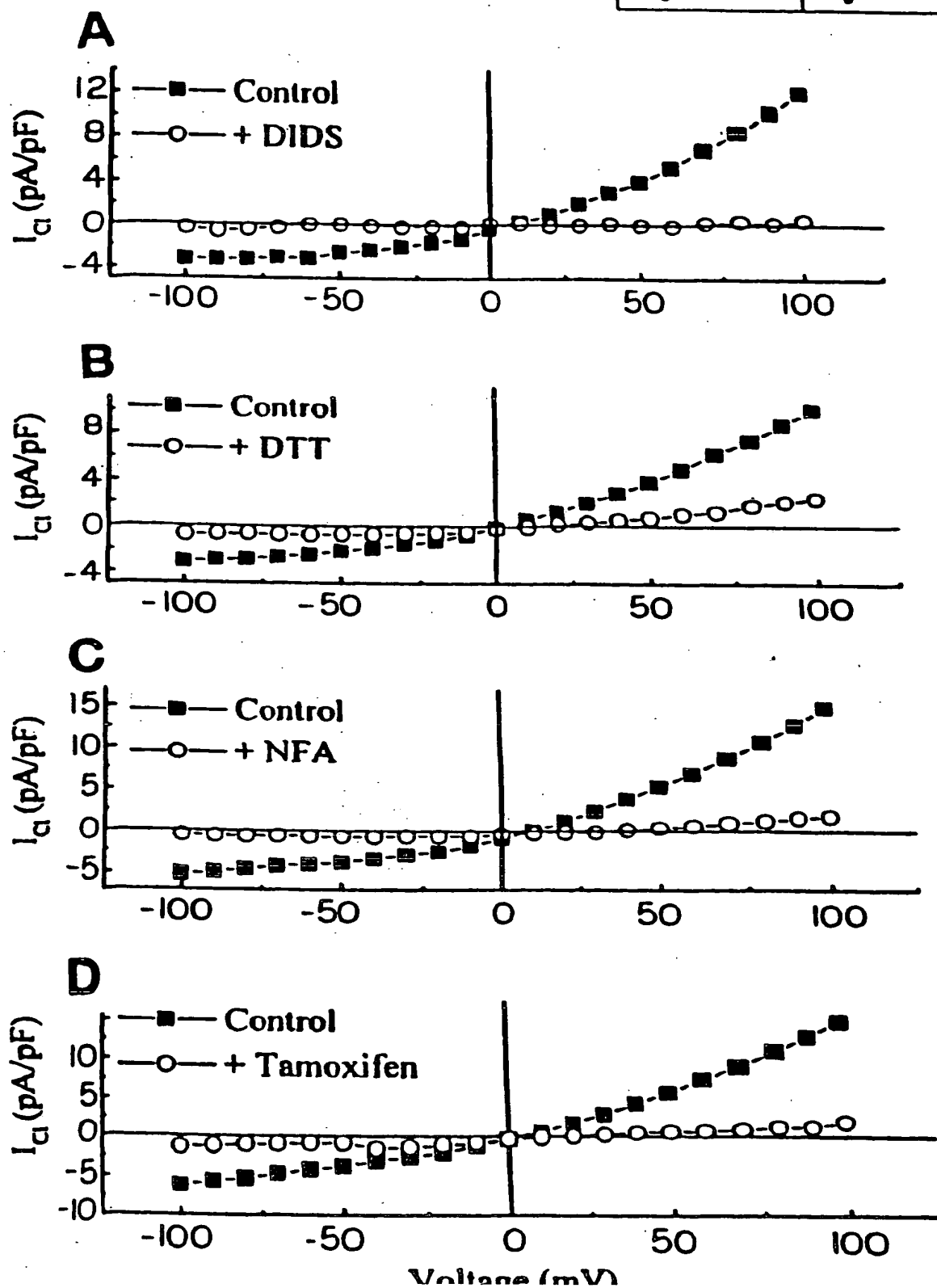


Figure 12

Figure 13

Figure 13A | Figure 13B



**E**

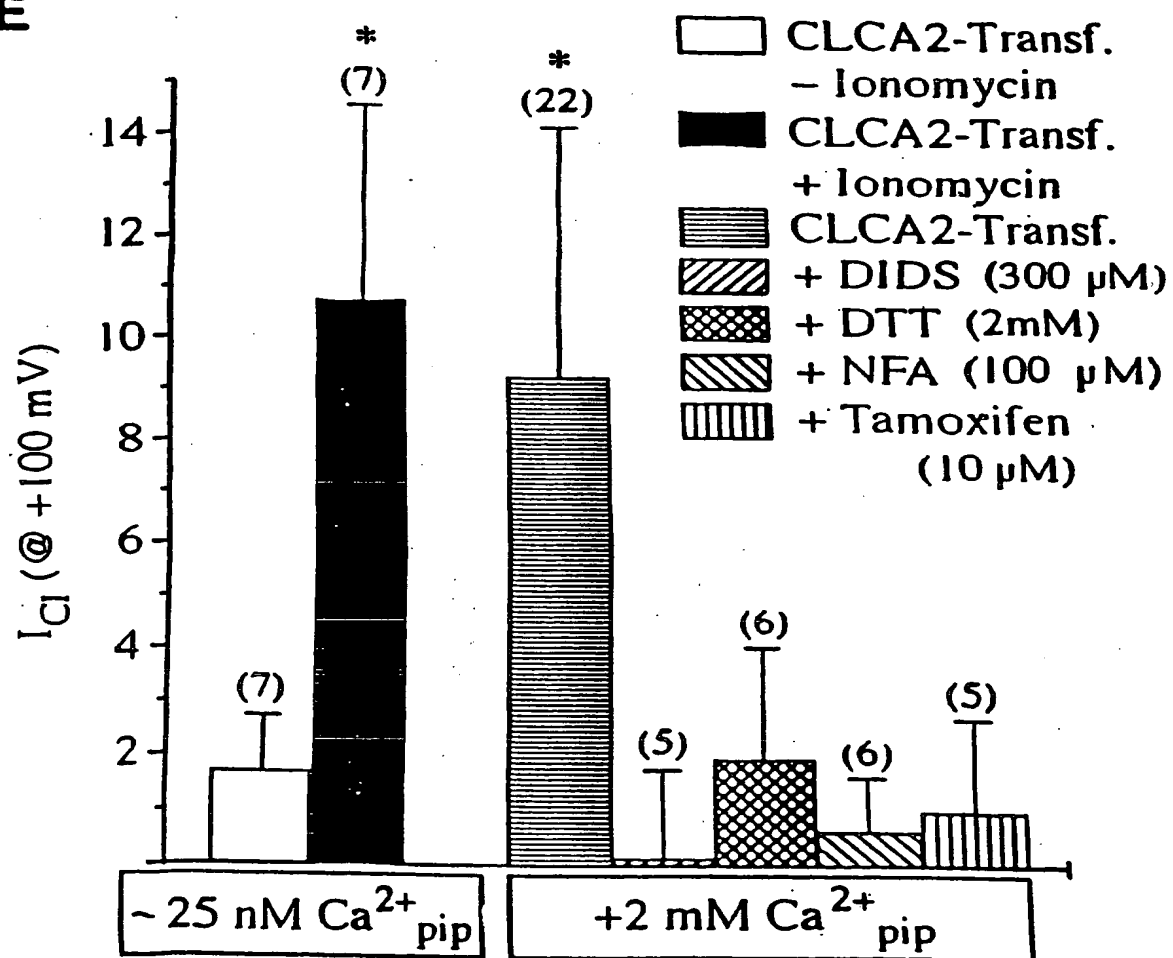


Figure 13B

Figure 14A

Figure 14

Figure 14A

Figure 14B

S	
h CLCA2	MTQSIAGPICNLKFVTLVALSSSELPFLGAGVQLQDNGYNGLLIAINPQVPENQNLSNIKEMITEASFYLFNATKRRV 80
h CLCA1	.GPFKSS-----VFILI.HL-.EGA.S--NSLI.NN...E.IVV.D.N...DET.QQ.D.V.Q.L...E..GK.F 72
b CLCA1	.VP.LTV-----IL.L..HL-.PG-MK--SSM.N.IN...D.IV...S..DEK.Q...V...T...H..... 71
Lu-ECAM-1	.VLCLNV-----IL.L..HL-.PG-MK--SSM.N.IN...D.IV...S..DEK.E...V...T...H..... 71
m CLCA1	.VPGLV-----L.L..HL-.QN-TE--SSM.H.NS...E.VV...S...DER.PS...V.Q.T...E.SQG.. 71
*	
h CLCA2	FFRNIKILIPATWKANN--SKIKQESYEKANVIVTDWYGAGHGDPPYTLQYRGCCKGEGKYIHFTPNFLNDNLTAGYSGRG 159
h CLCA1	.Y.K.VA...E...TKADYVRP.L.T.KN.D.L.AESTPPGN.E...E.MGN...EK.ER..L.D.IAGKK.AE--PQ. 151
b CLCA1	.Y...VS...M...SKSEYLP...DQ.E...ANP.LK...GR.EK.Q...TN.PI... 150
Lu-ECAM-1	.Y...VS...M...SKSEYFIP...DQ.D...ANP.LKY...GR.EK...TN.FHI... 150
m CLCA1	.Y...S.V.M...SKSEYLP.R...D.D...A.PHLQ...GQ.DR.Q...T...RI...P... 150
1 *	
h CLCA2	RVFVHEWAHLRWGVFDEYNNDKPFYINGQNIKVTRCSDITGIFV---CEKGPCPOENCIIISK---LFKEGCTFIYNS 232
h CLCA1	.KA.....EK...LS-NGR.QAV...AG...TN.V-KK.QG.S.YTKR.TFN.VTG.YEK..E.VLQ. 229
b CLCA1	.A.....I...G.Q...SRR.T.EA...TH...TN.IVK-QG.S.ITRP.RRDSQTG.YEAK...PEK 229
Lu-ECAM-1	.I.....V.Q...SRK.T.EA...TH...N.VFKK.PG.S.ITSL.RRDSQTG.YEAK...LPKK 230
m CLCA1	.....V.R...SRK.T.EA...AS...KK.V-HE.QR.S.VTRA.RRDSKTR.YEPK...PDK 229
1 *	
h CLCA2	TQNTASIMFMQSLSSVVEFCNASTHNQEAAPNLQNMCSLRSANDVITDSADFHHSFPMNGTELPPPTFSLVQAGDKVV 312
h CLCA1	.R.TEK...A.HVD.I...TEQN.K...K...K.N...T.E.R.E..KKT.TT-Q.N...L.I.QRI. 307
b CLCA1	.S.T.RE...H...T.TEK...V...K...K.NGK.T...MN.T.QNTS.TENMP.TQ...LKSQR.. 309
Lu-ECAM-1	.S.T.KE...P.H...T.TEK...T...K...K.NGK.T...MN.V.QNTS.TENMP.TH...LKSQR.. 310
m CLCA1	.I.T.G...N.N...TENN.A...K.NR..T...KT...QNA.P.R...A...Y.LKSRRR.. 309
:	
h CLCA2	CLVLDVSSKMAEADRLQLQQAEEFYLMQIVEIHTFVGIAFSKGEIRAQLHQHNSNDRKLLVSYLPTTVSAKTDISI 392
h CLCA1	....K.GS..TGN..NR.N..GOLF.L.T..LGSW..MVT...AAHVQSE.I...GS..DT.AKR..AA--SGGT.. 385
b CLCA1	....K.GS.SSE...FRMN...LF.I..I.KGSL..MVT...VA...NN.TK.TDDNVYENITAN..QE--NGGT.. 387
Lu-ECAM-1	....K.GS.SAE...F.MN...L.I.VI.KGSL..MVT...VA..QNH.TR.TDDNVYQKITAK..QV--NGGT.. 388
m CLCA1	....K.GS.DKE...IRMN...L.T...KESM..LVT...AAH.QNY.IK.T.SS.YQKITAN..QQ--SGGT.. 387
2	
h CLCA2	CSGLKKGFEVVEKNGKAYGSVMILVTSGDDKLLGNCLPTVLSSGSTIHSIALGSSAAPNLEELSRLTGGLKFFVPDISN 472
h CLCA1	....RSA..-T.IRKKYPTD..EIV.L.D.E.NTISG.FNE.KQ..AI..TV...P...QE...KM...QTYAS.QVQ 464
b CLCA1	.R...A..QAIIQSQSTS..EI..L.D.E.NEIH.S.IEE.KQ..VI..T...P...KE..T..DM...HR.YANKDI- 466
Lu-ECAM-1	.R...A..QAIIHSQSTS..EI..L.D.E.NEINS.FED.KR..AI..T...P...KE..T..NM...YR..ANKDI- 467
m CLCA1	.H..QA..QAITSQSTS..EIV.L.D.E.NGIRS.FEA.SR..AI..T...P.R.RE..T..DM...R.YANKDL- 466

h CLCA2	SNSMIDAFSRISSGTGDI	FOQHIOLESTGENV	KPHHQLKNTVTVD	TNGNDTMFLVTWQAS	GPPEIILFDPGRKY	TNN	552
h CLCA1	N.GL...	GAL...	N.AVS.RS...	K.LTLQNSQWMNG	I.S...K.L.I..	-TTQ.Q.L.W..S.Q.--QGG	541
b CLCA1	-GLTN...	RS.S.T..T...	KALAITKQWNG	P.S.I...F.V...	-TIKK...L.Q..K.K..K.SD	544	
Lu-ECAM-1	-TGLTN...	RS.S.T..A...	KALKITGRKRVNG	P.S...F.V...	-TIQK...V.Q..K.K..K.SD	545	
m CLCA1	-L...	TS.SVS..AL...	KAFD.RAGAWING	PL.S...F.VI..	-MVKK...Q..K.K..T.SD	544	
h CLCA2	FITN-LTERTASLWIPGTAK	PGHWTYTLNTHHS	LQALKVTVTSRAS	NSAVPPATVEAF	VERDSLHFPHPVMI	YANVKQG	631
h CLCA1	VVDK-NTKM.Y.Q...	I.V.T.K.S---	QA.S.T.TL...	ATL.I..TSKTNK	TSK..S.LVV...	IR..	617
b CLCA1	KEDK.NIHS.R.R...	I.ET.T...S.L.N.A.P.I.T...	T.RSPTT.V.AT	HMSQNTA.Y.S..IV..Q.S...	624		
Lu-ECAM-1	KEDK.NI.S.R.Q...	I.ET.T...S.L.N.A.S.M.T...	T.RSPTI..VIAT	HMSQHTA.Y.S.MIV..Q.S...	625		
m CLCA1	QDDK.NI.S.R.Q...	ET.T...SY--GTKS	LITM...T.RSPTME	LLGYCYMSQSTAQY	SRMIV..R.S...	622	
h CLCA2	FYPILNATVTATVEPETGDP	VTILRLDDGAGAD	VIKNDGIYSRYFFS	FAANGRYSLKVHVNH	SPSISTPAHSIPG	SHAMY	711
h CLCA1	AS...R.S...	LI.SVN.KT...	E.E.N...AT.D.V...	TTYDT...V..RALGGVNA	ARRRVIPOQ.G.L.	697	
b CLCA1	L.V.GIN...	II.T.D.HQ...	E.W.N...TV...	TDYRG...	AEARNNTARLSL	RQ.QNK.L. 704	
Lu-ECAM-1	L.V.GIS.I.II.T.D.HQ...	E.W.N...R.TV...	TDYVG...	AQARNNTARLN	RQ.QNKVL. 705		
m CLCA1	L.V.G.N...	LI.A.H.HQ...	E.W.N...IV...	TDYHG...	R.QAQRNKTRLSL	RQ-KNKSL. 701	
h CLCA2	VPGYTANGNIQMNA	PRKSVGRNEERK	WKG-FSRVSSGG	SFVLG-VPAGHPD	VPFPCKIIDLEA	-VKVEEELT	SWTAP 788
h CLCA1	I...WIE.DE...	W.P..PEINKDDVQH	QVC...T...-ASD	NA.I..L...GQ.T.K	EIHGGSLIN.T...	776	
b CLCA1	I...IE.K.IL.P...	PE.KDDLAKAEIED	LT...T.S.AP.-N..S.L.N...	...KE.ED-HIQ...	782		
Lu-ECAM-1	...VE.K.IL.P...	PE.KDDLAKA.IED	LT...T.S.AP.P.N..S...	...KE.ED-YIQ...	784		
m CLCA1	I...VE.K.VL.P...	PD.QEEAI	ATVED.N.T...T.S.AP.D.D	AR...S.VT...EFIGD	-YIH.T... 780		
h CLCA2	GEFDDQGQATS	YEIRMSKSLQNIQDD	FNNAILVNTSKRNP	QQAGIREIFTFSPQ	ISTNGPEHPNGETH	SHRIYVAIRA	868
h CLCA1	.D.Y.H.T.HK.I..I.T	ILDLR.K.ESLQ...	TALI.KE.NSE.V.L.K	ENI..-----FENGTD	LFI..Q. 846		
b CLCA1	ANVL.K.K.N..I..I...	FLDL.K.D.T...	SLK.KE..SD.N.E.K	EPFR-----IENG	TNF.I.VQ. 852		
Lu-ECAM-1	.NVL.K.K.N..I..I...	FMDR.E.D.T...	NLI.KE..SK.N.E.K	EHFR-----VENGT	KF.ISVQ. 854		
m CLCA1	.KVL.N.R.HR.I...	QHPLDL.E...T...	A.SLI.KE..SK.A.K.K	ETFK-----IANGI	QL.I..Q. 850		
h CLCA2	MDRNSLQSAVSNIAQAP	LFIPPNSDP-VPARD	YLILKGVLTAMGLIG	ICLIIVVTHHTLSR	KKRA	DKKENGTKLL 943	
h CLCA1	V.KVD.K.EI...	RVS...QTP.ET.SP	-----ETSAPCPN	-H.NST.PGIHILKIMW	WIG---	LQLSIA 914	
b CLCA1	INEAN.T.E...	IK...MP-----EDSV	P.L.-TK.SAINLA	IFALAMI-----LSIV	904		
Lu-ECAM-1	INEAN.I.E..H.V	IK...LP-----EDSV	HDL.-TK.SEITLAIL	GLPMI-----FSV-F	905		
m CLCA1	DNEA..T.E...	VKLTSL-----EDSIS	L.-DD.SAISMTINGL	VI-----FNSI	N 902		

Figure 14B

Fig. 15A

# GST-bCLCA2 Fusion Proteins

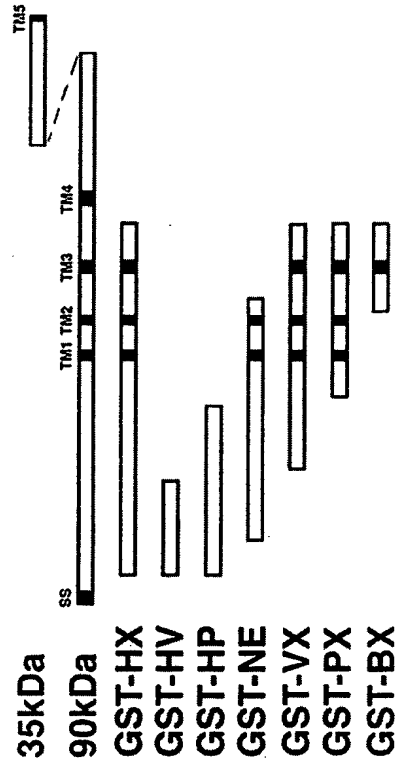


Fig. 15B

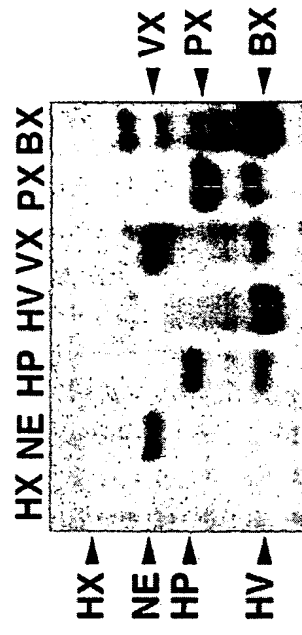


Fig. 15C

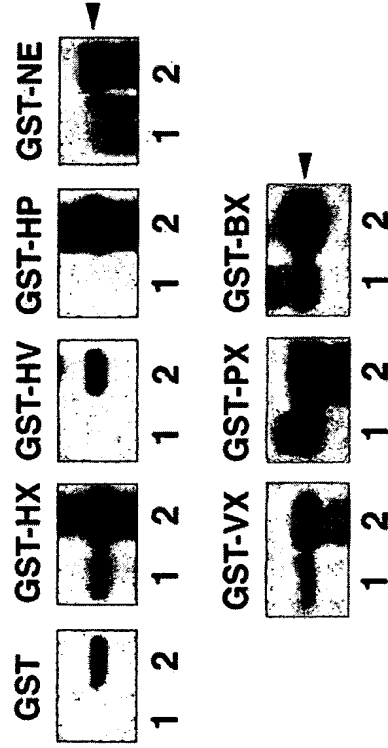


Fig. 15D

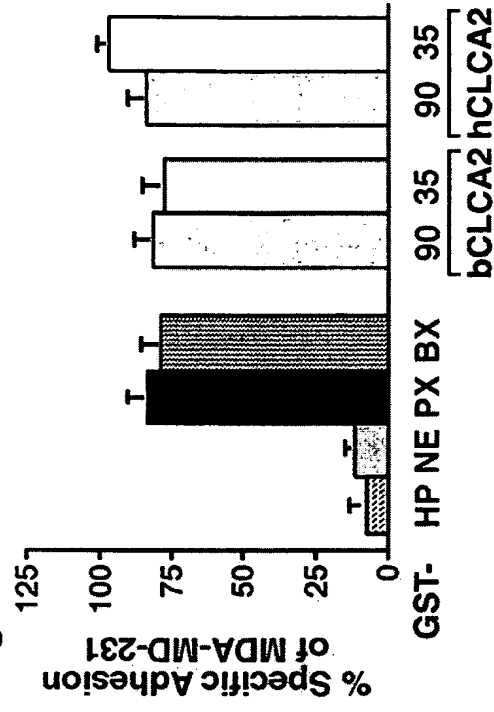




Fig. 16A

	90-kDa	35-kDa
hCLCA2	<b>AFSRISSGTG</b>	<b>GFSRVSSGGS</b>
mCLCA5	<b>AFVRISSGTG</b>	<b>GFSRVSSGGS</b>
mCLCA1	<b>AFSRISSSTG</b>	<b>DFNRVTSGGS</b>
bCLCA2	<b>AFSRISSRSG</b>	<b>DFSRLTSGGS</b>

Fig. 16B

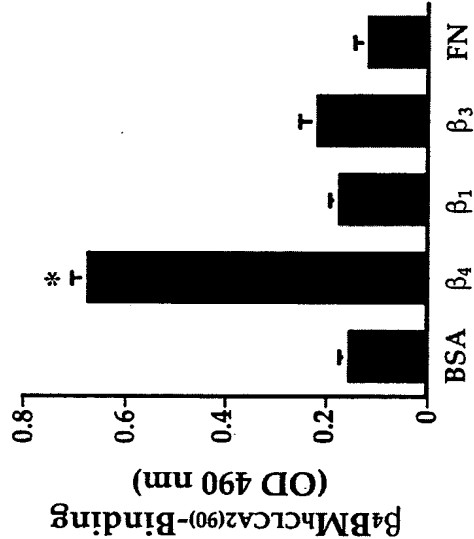


Fig. 16C

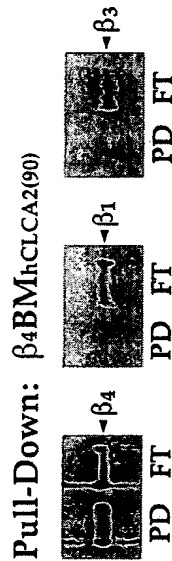


Fig. 16D

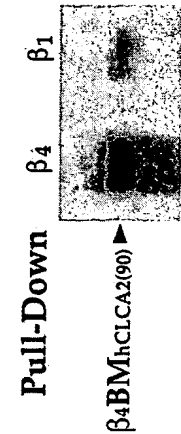


Fig. 17A

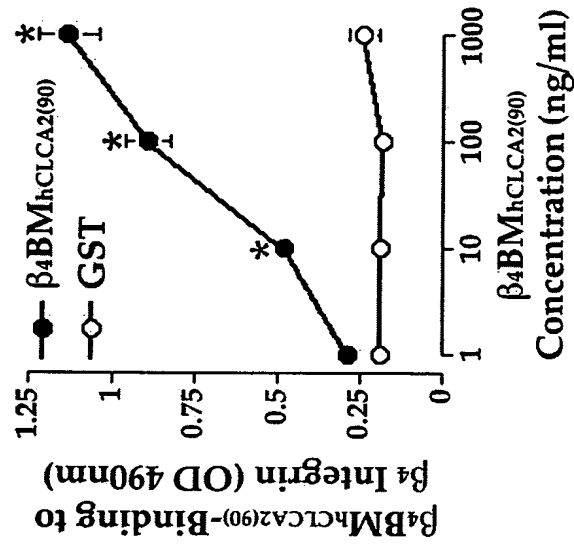


Fig. 17B

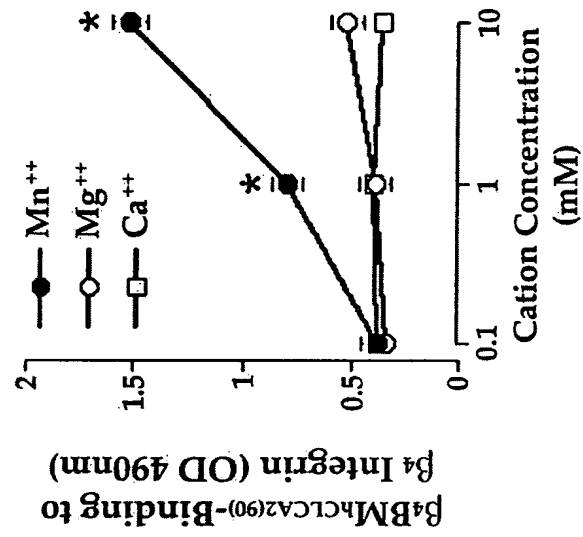


Fig. 17A

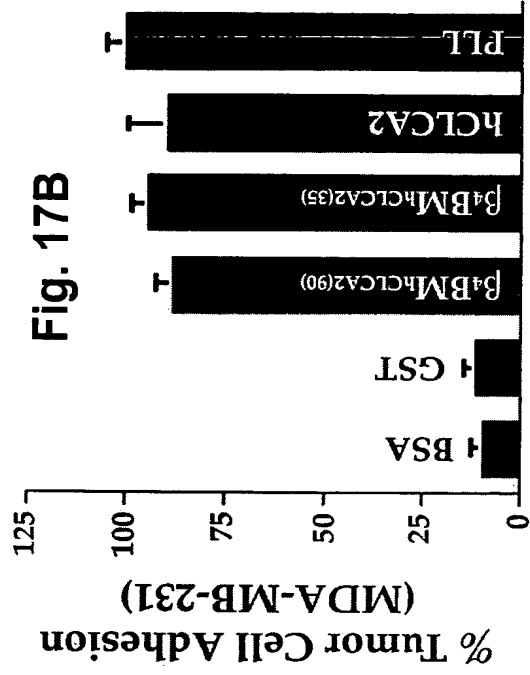
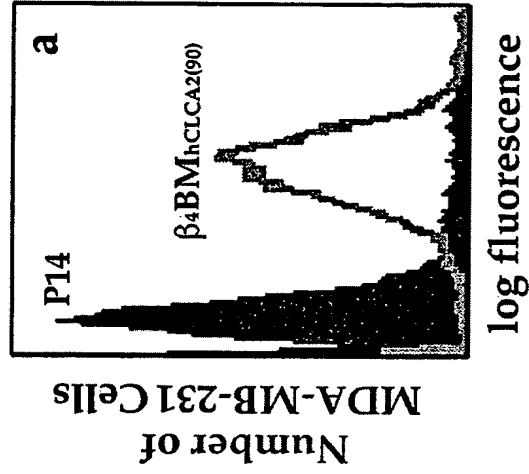
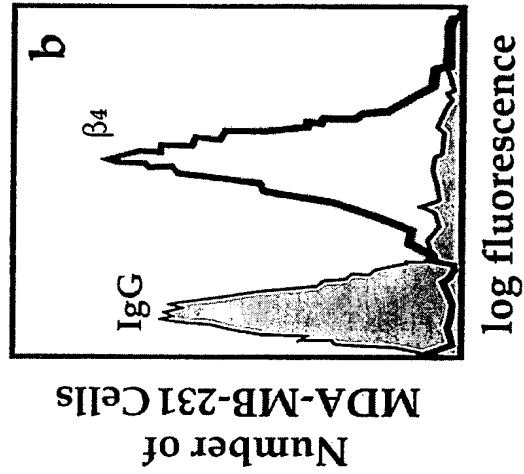
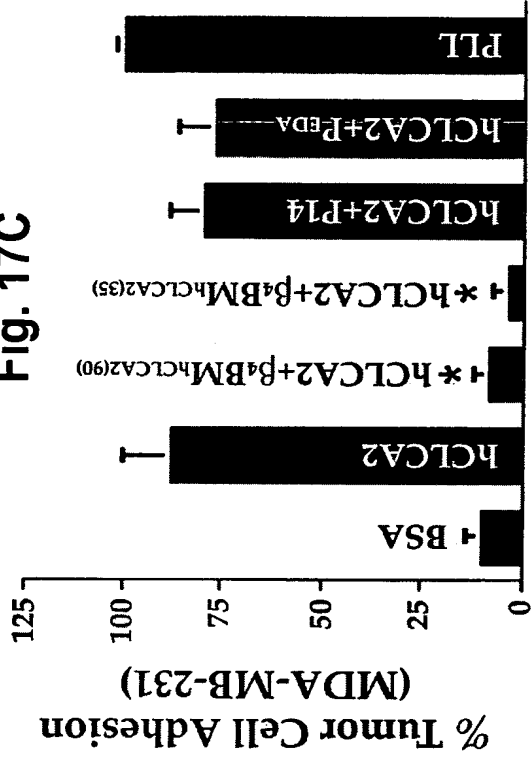
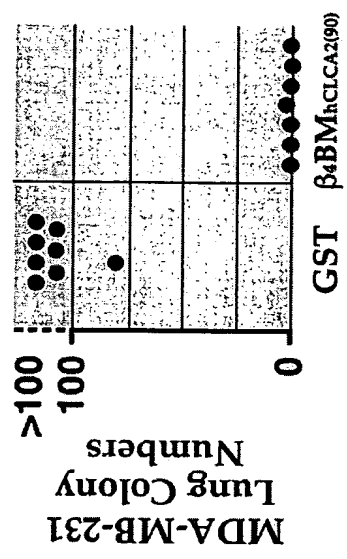
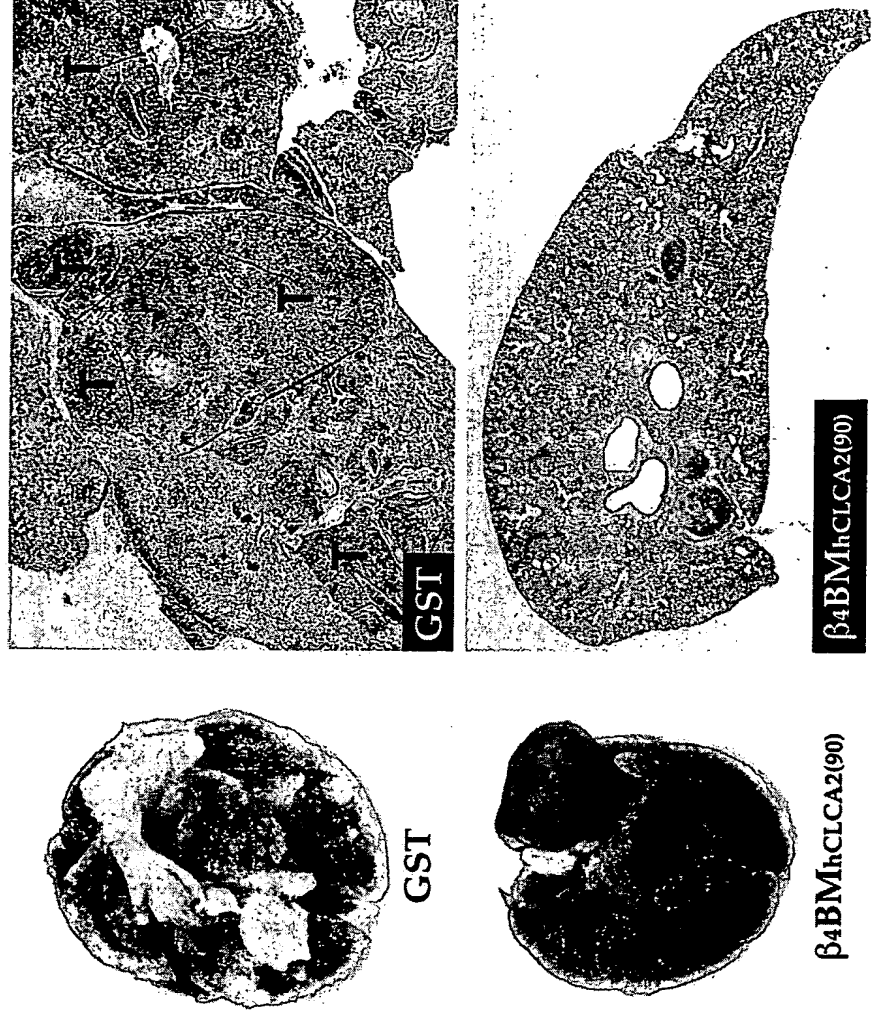


Fig. 17C



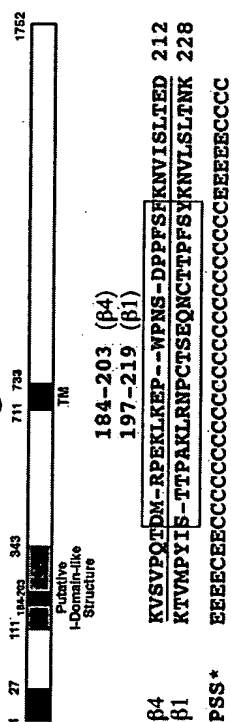


**Fig. 19A**

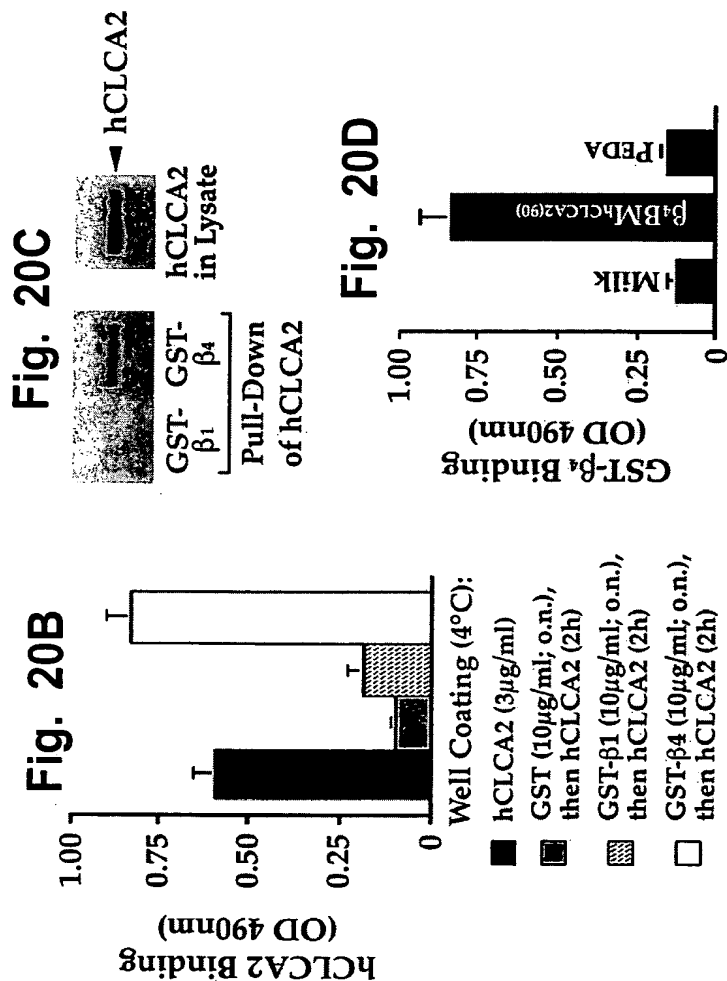


**Fig. 19B**

**Fig. 20A**

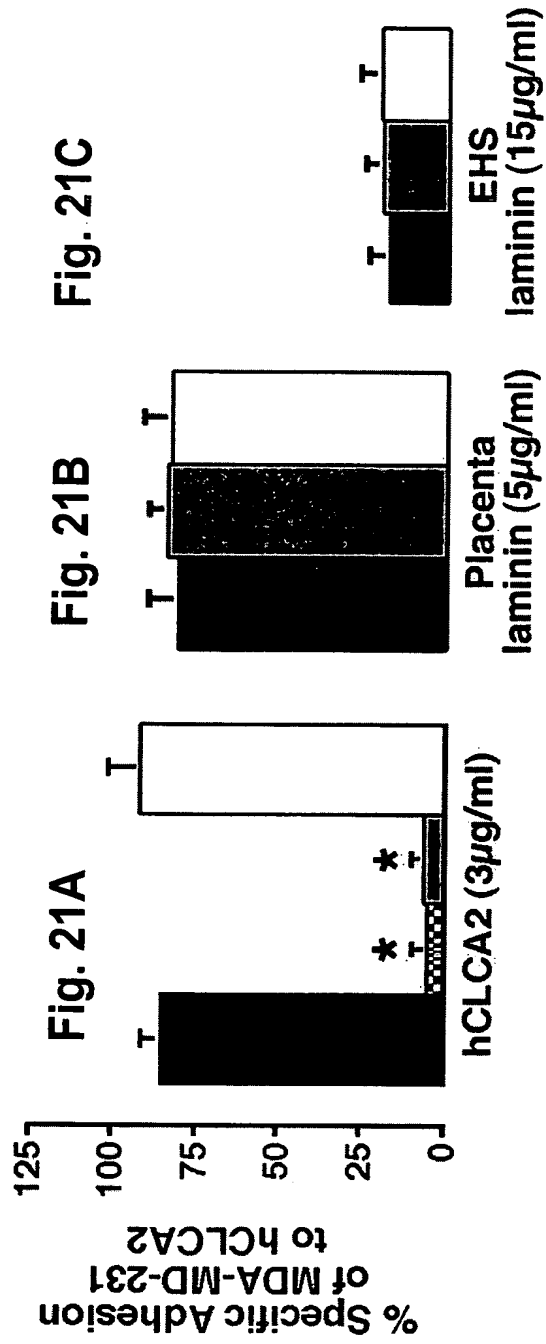


\* Predicted Secondary Structure: E, sheet; C, coil. (see ref. 27)

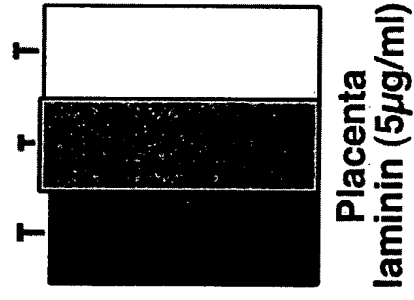


**Fig. 20E**

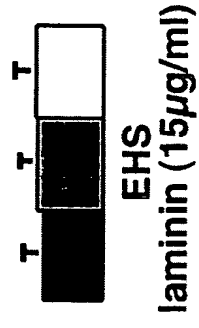




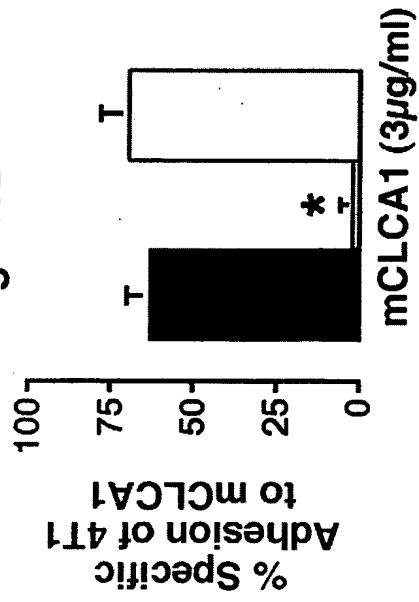
**Fig. 21B**



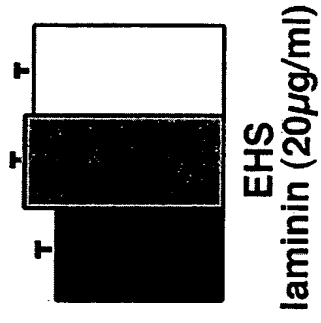
**Fig. 21C**



**Fig. 21D**



**Fig. 21E**



■ Substrate alone   
 ■ in the presence of  $\beta_4$ -peptide   
 ■ blocked with  $\beta_1$ -peptide   
 ■ blocked with  $\beta_4$ -peptide

Fig. 22A

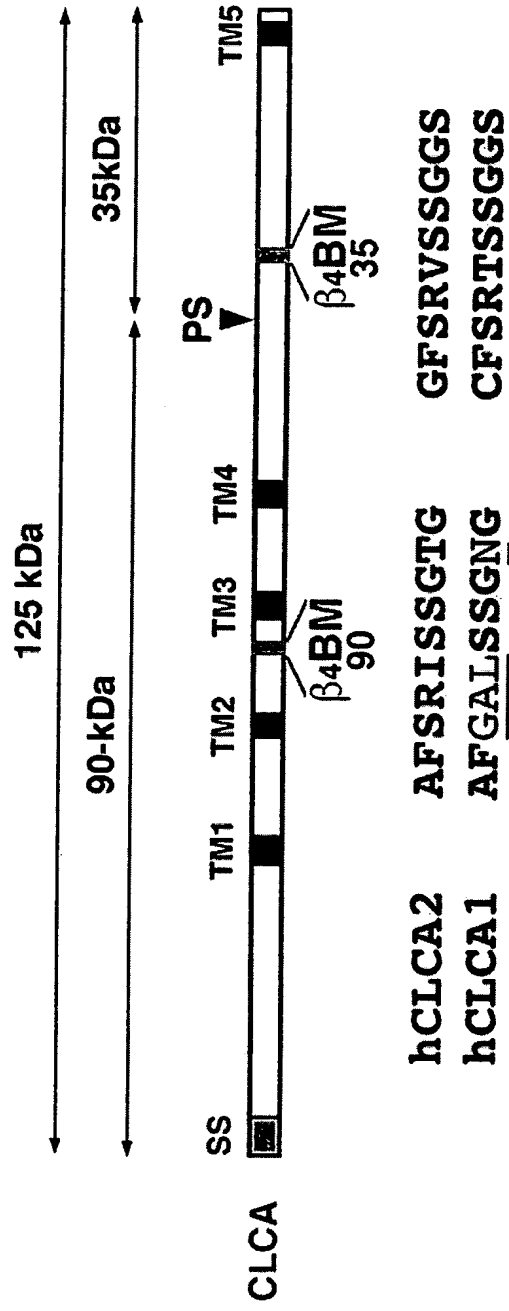


Fig. 22B

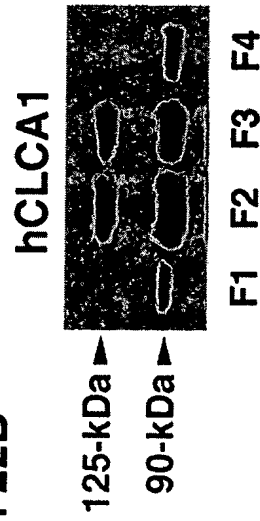


Fig. 22D

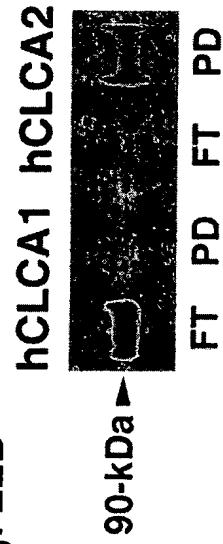


Fig. 22C

